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Androgens Induce Functional CXCR4 through ERG Factor Expression in TMPRSS2-ERG Fusion-Positive Prostate Cancer Cells[1,2]

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Abstract

TMPRSS2-ERG fusion transcripts have been shown to be expressed in a majority of prostate cancer (PC) patients because of chromosomal translocations or deletions involving the TMPRSS2 gene promoter and the ERG gene coding sequence. These alterations cause androgen-dependent ERG transcription factor expression in PC patients. We and others have shown that chemokine receptor CXCR4 expression is upregulated in PC tumor cells, and its ligand, CXCL12, is expressed in bone stromal cells. The CXCL12/CXCR4 axis functions in PC progression to enhance invasion and metastasis. To address the regulation of CXCR4 expression, we identified several putative ERG consensus-binding sites in the promoter region of CXCR4. We hypothesized that androgen-dependent regulation of the ERG transcription factor could induce CXCR4 expression in PC cells. Results of the current study show that 1) prostate tumor cells coexpress higher ERG and CXCR4 compared with benign tissue, 2) CXCR4 expression is increased in the TMPRSS2-ERG fusion–positive cell line, 3) ERG transcription factor binds to the CXCR4 gene promoter, 4) synthetic androgen (R1881) upregulates both ERG and CXCR4 in TMPRSS2-ERG fusion–positive VCaP cells, 5) small interfering RNA–mediated down-regulation of ERG resulted in the loss of androgen-dependent regulation of CXCR4 expression in VCaP cells, and 6) R1881-activated TMPRSS2-ERG expression functionally activates CXCR4 in VCaP cells. These findings provide a link between TMPRSS2-ERG translocations and enhanced metastasis of tumor cells through CXCR4 function in PC cells.

Translational Oncology (2010) 3, 195–203

Introduction

Specific chromosomal alterations were recently discovered in prostate cancer (PC) patients using bioinformatics analysis of microarray data [1,2]. Prevalent chromosomal alterations due to interstitial deletion or translocations result in the fusion of the androgen-responsive TMPRSS2 gene promoter with Ets transcription factor coding sequences. The Ets family of transcription factors ERG, ETS translocation variants 1 and 4 (ETV1 and ETV4), were shown to be involved in chromosomal alterations. Among these transcription factors, ERG was identified as being commonly fused with the *TMPRSS2* gene in most PC patients [1–3]. Some reports suggest that the presence of fusions is associated with a poor outcome [4–6] and that specific ERG isoform expression correlates with aggressive disease characteristics [7]. Other studies suggest that these chromosomal alterations alone are not associated with patient outcome but that copy number increase of the alterations results in poor outcomes [8]. Previous reports demonstrate that prostate-specific overexpression of the *ERG* gene in transgenic mouse models results in the development of prostate intraepithelial neoplasia (PIN) without progression to carcinoma [9,10]. TMPRSS2-ERG translocations have also been identified in the low-grade PIN lesions adjacent to cancer, suggesting that ERG expression contributes to PIN development [11]. Further, two recent

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reports demonstrate that ERG overexpression alone is not sufficient for PC progression; additional loss of PTEN co-operates in the development of highly invasive prostate adenocarcinoma [12,13]. Studies with patient tumor tissues confirmed *in vivo* findings that alterations in *ERG* and *PTEN* genes in PC patients result in the development of aggressive disease [14]. The molecular targets related to androgen-mediated activation of TMPRSS2-ERG are currently unknown; herein, we provide evidence that the chemokine receptor CXCR4 is one such target of androgens in PC cells.

CXCR4 is a chemokine receptor that has been shown to function as a key receptor for homing of circulating tumor cells to secondary sites; its ligand CXCL12 is highly expressed at these metastatic sites [15–17]. CXCL12/CXCR4 signaling has been shown to be involved in the adhesion, migration, invasion, and metastasis of PC cells in laboratory model systems [16,17]. We have recently shown that CXCL12/CXCR4 signaling transactivates members of the epidermal growth factor receptor family in membrane microdomains of PC cells, and this transactivation contributes to the expansion of intraosseous metastatic deposits [18]. CXCR4 has been shown to be deregulated in tumor cells through transcriptional mechanisms. Prostate tumors and metastases express higher levels of CXCR4 compared with nontumor tissue [19–21], and this overexpression is associated with aggressive disease in patients [20,22].

A recent study suggests that *CXCR4* is one of the functional target genes for ERG transcription factor in PC cells [12]. To determine the link between TMPRSS2-ERG translocations and CXCR4 expression in PC cells, we investigated the role of androgens in the activation of TMPRSS2-ERG and the subsequent expression of CXCR4 in PC cells. Herein, we show that PC cells that exhibit TMPRSS2-ERG fusions have androgen-regulated CXCR4 expression and that knock down of ERG abrogates androgen-induced CXCR4 expression. Furthermore, the CXCR4 promoter contains several putative ERG binding sites, and the ERG factor binds to the CXCR4 promoter in TMPRSS2-ERG–positive VCaP cells. Androgens and CXCL12 independently induced chemoinvasion of VCaP cells, and in combination, they induced chemoinvasion in an additive manner. CXCR4 inhibition studies suggest that androgen-induced CXCR4 expression is functional in TMPRSS2-ERG–positive PC cells. These studies provide an important link between TMPRSS2-ERG chromosomal translocations and androgen-induced CXCR4-mediated metastasis formation.

Materials and Methods

Cell Culture

VCaP, PC-3, and LNCaP cells were purchased from American Type Culture Collection (Manassas, VA). PC-3 and LNCaP cells were cultured in RPMI 1640 medium, and VCaP cells were cultured in Dulbecco's modified Eagle medium. All cell lines were tested for *Mycoplasma* contamination before use in the experiments with VenorGeM Mycoplasma detection kit from Sigma Biochemicals (St Louis, MO). The culture medium was supplemented with 10% fetal bovine serum and 1% penicillin and streptomycin. R1881 was purchased from NEN Life Sciences (Waltham, MA), flutamide and cycloheximide were purchased from Sigma, and CXCL12 was purchased from Peprotech (Rocky Hill, NJ).

Quantitative Polymerase Chain Reaction

A total of 4×10^5 cells were seeded in six-well plates. Each plate was treated with a single agent of an androgen agonist R1881, antagonist flutamide, or cycloheximide or with a combination of R1881 with flutamide or cycloheximide as shown in figure legends. Total RNA was isolated using the TRIzol reagent (Invitrogen, Carlsbad, CA). For reverse transcription–polymerase chain reaction (PCR) studies, first-strand complementary DNA was synthesized from 2 μg of total RNA with an oligo(dT) primer and SuperScript II Reverse Transcriptase (Invitrogen). Forward and reverse primers were designed using the Primer 3 program (http://frodo.wi.mit.edu/cgi-bin/primer3/primer3_www.cgi). The forward and reverse primers are as follows: for ERG, 5′-AAC GAG CGC AGA GTT ATC GT-3′ and 5′-GTG AGC CTC TGG AAG TCG TC-3′; for CXCR4, 5′-GGC CCT CAA GAC CAC AGT CA-3′ and 5′-TTA GCT GGA GTG AAA ACT TGA AG-3′; for prostate-specific antigen (PSA), 5′-GGT GAT GAC TCC AGC CAC GA-3′ and 5′-GCG CAC ACA CGT CAT TGG AA-3′; and for glyceraldehyde 3-phosphate dehydrogenase (GAPDH), 5′-AAG GTC ATC CCT GAG CTG AA-3′ and 5′-TGA CAA AGT GGT CGT TGA GG-3′. Real-time PCR analysis was performed with SYBR Green PCR core reagents (Stratagene, La Jolla, CA) in a Stratagene Mx4000 cycler, and data analysis was performed using Mx4000 v3.01 software. All primer sets were tested in real-time PCR and found to produce no detectable peaks in dissociation curves due to primer-dimer amplifications. Relative message levels were calculated with a comparative C_t (threshold cycle) method [23]. Briefly, message levels were normalized to endogenous GAPDH message levels. In treated samples, relative quantitation was performed by the comparative C_t method [23] using the formula $2^{-\Delta\Delta}C_t$, where $\Delta\Delta C_t = [C_t \text{ test gene (treated sample)} - C_t \text{ GAPDH (treated sample)}] - [C_t \text{ test gene (control sample)} - C_t \text{ GAPDH (control sample)}]$. For each sample, real-time PCR was performed in triplicate samples. C_t represents the mean C_t value of each sample, and GAPDH is the endogenous control used to normalize the quantification of a test gene.

Secondary Data Analysis for ERG and CXCR4 Expression in Human Benign Prostate and Prostate Cancer Tissue

Expression profile data sets for human benign and PC tissue were queried for ERG and CXCR4 expression using the Gene Expression Omnibus database (http://www.ncbi.nlm.nih.gov/geo/). This record was deposited by Yu et al. as previously described [24]. We extracted the gene expression values for ERG and CXCR4 for benign prostate (n = 18) and PC tissue (n = 65) from GDS2546 record. ERG and CXCR4 expression values were analyzed with GraphPad Prism software version 3.0 (GraphPad, San Diego, CA).

Western Blot Analysis

Subconfluent cultures of VCaP cells were washed with phosphate-buffered saline, and total cellular proteins were extracted with buffer containing 62.5 mM Tris-HCl (pH 6.8), 2% SDS, 1 mM PMSF, and 1 × Protease inhibitor cocktail (Roche, Indianapolis, IN). Protein content was quantified with a BCA protein assay (Pierce Biotechnology, Inc, Rockford, IL), and equal amounts of protein were resolved by 10% SDS-PAGE. Immunoblot was performed with antibodies to ERG (Santa Cruz Biotechnology, Santa Cruz, CA), CXCR4 (Millipore, Billerica, MA), and GAPDH (Trevigen, Gaithersburg, MD). After secondary antibody incubation, chemiluminescence reaction was performed with SuperSignal Western Femto or Pico Substrate (Pierce Biotechnology, Inc). The band intensities were determined by quantitation of pixel intensities using Un-Scan-It software (version 5.1; Orem, UT). Apparent molecular weights of ERG forms were also determined by Un-Scan-

It software using a reference position of molecular weight markers in the radiographs.

Fluorescence-Activated Cell Sorting Analysis

Fluorescence-Activated Cell Sorting Analysis (FACS) was performed on VCaP cells as previously described [17]. Briefly, VCaP cells grown in culture plates were scraped and counted on hemocytometer. A total of 5×10^5 cells were resuspended in phosphate-buffered saline supplemented with 5% fetal bovine serum and incubated with either phycoerythrin (PE)-conjugated anti-CXCR4 antibody (BD Pharmingen, San Diego, CA) or isotype-matched IgG_{2a} (BD Pharmingen) for 15 minutes on ice. Antibody-bound cancer cells were washed three times and analyzed on fluorescence-activated cell sorter (Becton Dickinson, San Diego, CA). CXCR4-positive cells were enumerated using the cell quest software (Becton Dickinson). Data shown are percent of total gated cells that are positive for anti–CXCR4-PE antibody binding.

Chemoinvasion Assay

VCaP cells were serum-starved for 4 hours. A total of 1.5 to 2.0 × 10^5 cells were seeded onto inserts in the upper chamber of transwell culture plates (Becton Dickinson). Before seeding, the inserts were precoated with Matrigel. To activate the androgen receptor (AR), 0.5 nM of R1881 was added to the upper chamber. CXCL12 was placed in the bottom chamber for CXCR4-mediated chemoinvasion. Cell invasion was allowed to proceed for 24 hours. Later, the upper chambers were cleaned with cotton swabs to remove nonmigrated/invaded cells, and the inserts were stained with Diff-Quik stain set (Dade Behring, Inc, Newark, DE). The total number of migrated cells in a high-power field was counted under a microscope, and the data presented are based on three independent experiments.

Chromatin Immunoprecipitation

The experiment was performed using a kit from Active Motif, Inc (Carlsbad, CA). As per the manufacturer's recommendations, subconfluent cultures of VCaP cells were fixed with 1% formaldehyde solution, sonicated to shear the chromatin, and incubated with anti-ERG or isotype IgG antibodies and protein G magnetic beads. The immunoprecipitates were washed to remove nonspecific complexes. Chromatin was then eluted by reverse cross-linking and was treated with proteinase K. PCR was performed with primers designed with 5′ sequences of CXCR4 and GAPDH promoters. The forward primer 5′-GGA TCC CCA ACG CCT AGA AC-3′ and reverse primer 5′-CAG CCC ATT CAG GAG GTA AA-3′ were used for CXCR4, and the forward primer 5′-TAC TAG CGG TTT TAC GGG CG-3′ and reverse primer 5′-TCG AAC AGG AGG AGC AGA GAG CGA-3′ were used for GAPDH in the PCR. PCRs were analyzed on 2% agarose gels.

Statistical Analysis

For CXCR4 and ERG expression, the Mann-Whitney test was performed between benign and PC tissue data. The Pearson correlation test was performed for CXCR4 and ERG expression in tumor samples, and the correlation coefficient, *r*, was determined using GraphPad Prism software version 3.0 (GraphPad). For *in vitro* chemoinvasion study, statistical significance was determined by the nonparametric analysis of variance test followed by the Tukey posttest to compare all pairs of a column. $P \leq .05$ was considered statistically significant.

Results

ERG and CXCR4 Coexpressed in PC Cells

CXCR4 expression in PC cells has been shown to contribute to secondary metastasis formation in bone tissue [18,25]. We identified several Ets transcription factor binding sites, including several consensus ERG transcription factor binding sites [26] in the promoter region of CXCR4 (Table W1). Binding of Ets factors to these sites potentially contribute to CXCR4 expression. To determine the role of TMPRSS2-ERG translocations on CXCR4 expression, we assessed ERG and CXCR4 expression in TMPRSS2-ERG fusion–positive VCaP cells, TMPRSS2-ERG fusion–negative PC-3 cells, and human prostate tumor tissues.

Secondary analysis of public domain expression array profile data of benign prostate and prostate tumor tissue [24] shows that both ERG and CXCR4 are expressed significantly higher in prostate tumor tissue samples (Figure 1*A*). Correlation studies with ERG and CXCR4 in prostate tumor samples show a moderate association between ERG and CXCR4 gene expressions ($r = 0.4238$ and $P < .001$). Similar ERG and CXCR4 expression patterns have been observed in the limited number of PC patient tumor tissues and the adjacent nontumor tissue available for investigation (data not shown). Together, these data suggest a concerted up-regulation of ERG and CXCR4 in tumor cells. Gene expression studies with cell lines show that both ERG and CXCR4 transcript levels are higher in VCaP cells compared with PC-3 cells (Figure 1*B*). Western blot analysis showed that ERG expression is not detectable in PC-3 cells, whereas in VCaP cells, ERG is expressed in two different forms. Similarly, the level of CXCR4 expression is significantly higher in VCaP cells compared with that in PC-3 cells (Figure 1*C*). To address whether ERG can regulate CXCR4 gene expression, we performed chromatin immunoprecipitation experiments with VCaP cells. These studies demonstrated that in VCaP cells anti-ERG antibodies immunoprecipitated ERG and CXCR4 gene promoter fragment complexes, whereas IgG failed to immunoprecipitate such complexes in VCaP cells (Figure 1*D*). Together, these data suggest that in TMPRSS2-ERG–positive cells, ERG and CXCR4 are highly expressed, and ERG binds with the CXCR4 promoter sequences in VCaP cells.

Androgens Regulate CXCR4 Gene through ERG Transcription Factor Expression in PC Cells

To determine whether R1881 regulation of *CXCR4* gene expression was mediated through the activation of TMPRSS2-ERG fusions, gene expression studies with VCaP, LNCaP, and PC-3 cells were performed. In the absence of R1881 stimulation, *CXCR4* was expressed in all cell types, whereas *ERG* expression was higher in VCaP cells compared with PC-3 and LNCaP cells (Figure 2*A*). R1881 treatment of VCaP cells induced both *ERG* and *CXCR4* messenger RNA expression (Figure 2*B*). As expected, synthetic androgens induced *PSA* expression in AR–positive VCaP and LNCaP cells but not in PC-3 cells that lack a functional AR. Synthetic androgen treatment enhanced both *ERG* and *CXCR4* expression in VCaP cells but not in AR–positive LNCaP cells. As expected, the antiandrogen flutamide abrogated the synthetic androgen induction of *PSA* in VCaP and LNCaP cells. Similarly, flutamide treatment also abrogated the androgen-induced ERG and CXCR4 expression in VCaP cells and CXCR4 expression in LNCaP cells

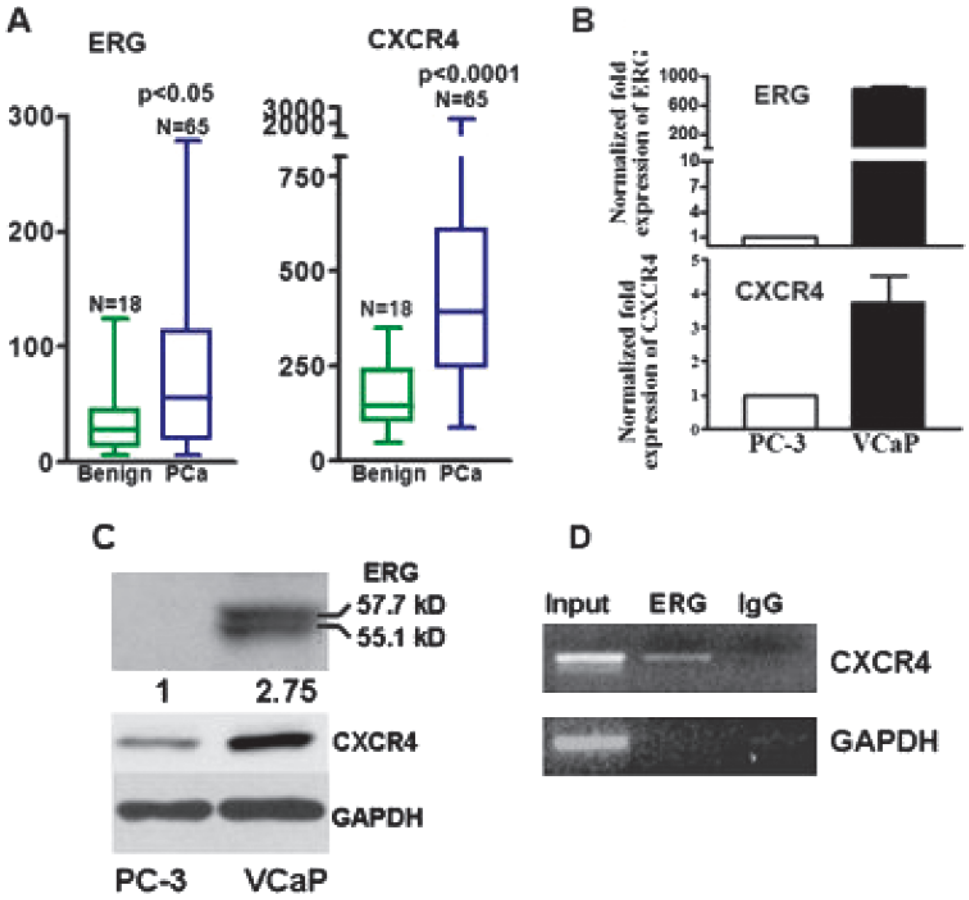

Figure 1. ERG and CXCR4 were highly expressed in TMPRSS2-ERG fusion–positive cell and prostate tumor cells, and ERG binds to CXCR4 promoter. (A) Expression array data for ERG and CXCR4 were obtained from GDS2546 record from Gene Expression Omnibus database. Mann-Whitney test was performed between samples to determine statistical significance. (B) Quantitative PCR analysis of *ERG* and *CXCR4* genes was performed with messenger RNA prepared from PC-3 and VCaP cells. The relative expressions of genes were shown after normalization with the housekeeping gene *GAPDH*. (C) Total cellular proteins were isolated from PC-3 and VCaP cells and immunoblotted with anti-ERG, anti-CXCR4, and anti-GAPDH antibodies. A representative radiograph of chemiluminescence detection is shown with multiple independent Western blot analyses. Apparent molecular weights of ERG forms are shown for VCaP cells. (D) Chromatin immunoprecipitation assay was performed with VCaP cell DNA with anti-ERG and isotype antibodies. Immunoprecipitated chromatin was amplified with *CXCR4* and *GAPDH* gene primers in the 5′region. Ethidium bromide–stained gel analysis of PCR-amplified DNA fragments is also shown.

(Figure 2*C*). The absence of androgen-induced ERG expression in LNCaP cells suggests that androgen-induced ERG transcriptionally regulates CXCR4 in VCaP cells.

To determine whether androgens regulate *CXCR4* expression, we treated VCaP cells with different concentrations of the synthetic androgen R1881 and measured cell surface *CXCR4* expression through FACS analysis. R1881 treatment upregulated cell surface *CXCR4* expression, and a higher concentration of R881 further enhanced *CXCR4* cell surface expression (Figure 3).

To further determine that *CXCR4* is an indirect target of androgens, we treated VCaP cells with the translational inhibitor cycloheximide. Vehicle- and cycloheximide-treated cells were analyzed for R1881 induction of *CXCR4* and *PSA* expression in VCaP cells. As expected, cycloheximide did not abrogate R1881 induction of *PSA* but inhibited the R1881 induction of *CXCR4* expression in VCaP cells (Figure 4). These data imply that R1881-induced new protein synthesis is required for CXCR4 expression in VCaP cells. Together, these data support the notion that R1881 activation of TMPRSS2-ERG translocations induces CXCR4 expression in PC cells.

ERG Is Required for CXCR4 Gene Expression in VCaP Cells

To confirm that the androgen-induced ERG transcription factor regulates *CXCR4* gene expression, we tested the effect of small interfering RNA (siRNA)–mediated down-regulation of the *ERG* gene. SiERG transfection resulted in the down-regulation of both *ERG* and *CXCR4* gene expression compared with scrambled siRNA transfection (Figure 5*A*). Western blot analysis show that a 60% inhibition of ERG protein expression compared with scrambled siRNA transfection (Figure 5*B*). To assess the role of androgens in the regulation of *CXCR4* expression, we treated the scrambled and siERG-transfected VCaP cells with synthetic androgens and measured the *CXCR4* gene expression (Figure 5, *B* and *C*). Synthetic androgens upregulated the *CXCR4* gene expression in scrambled siRNA-transfected cells but were unable to upregulate the *CXCR4* gene in siERG-transfected cells. As expected, synthetic androgens upregulated *PSA* expression in both cells (Figure 5*D*). These data imply that, although *PSA* is not a target for R1881-induced *ERG* expression, *CXCR4* is regulated by this mechanism. Taken together, these data demonstrate that the androgen-induced expression of ERG transcription factor regulates CXCR4 expression.

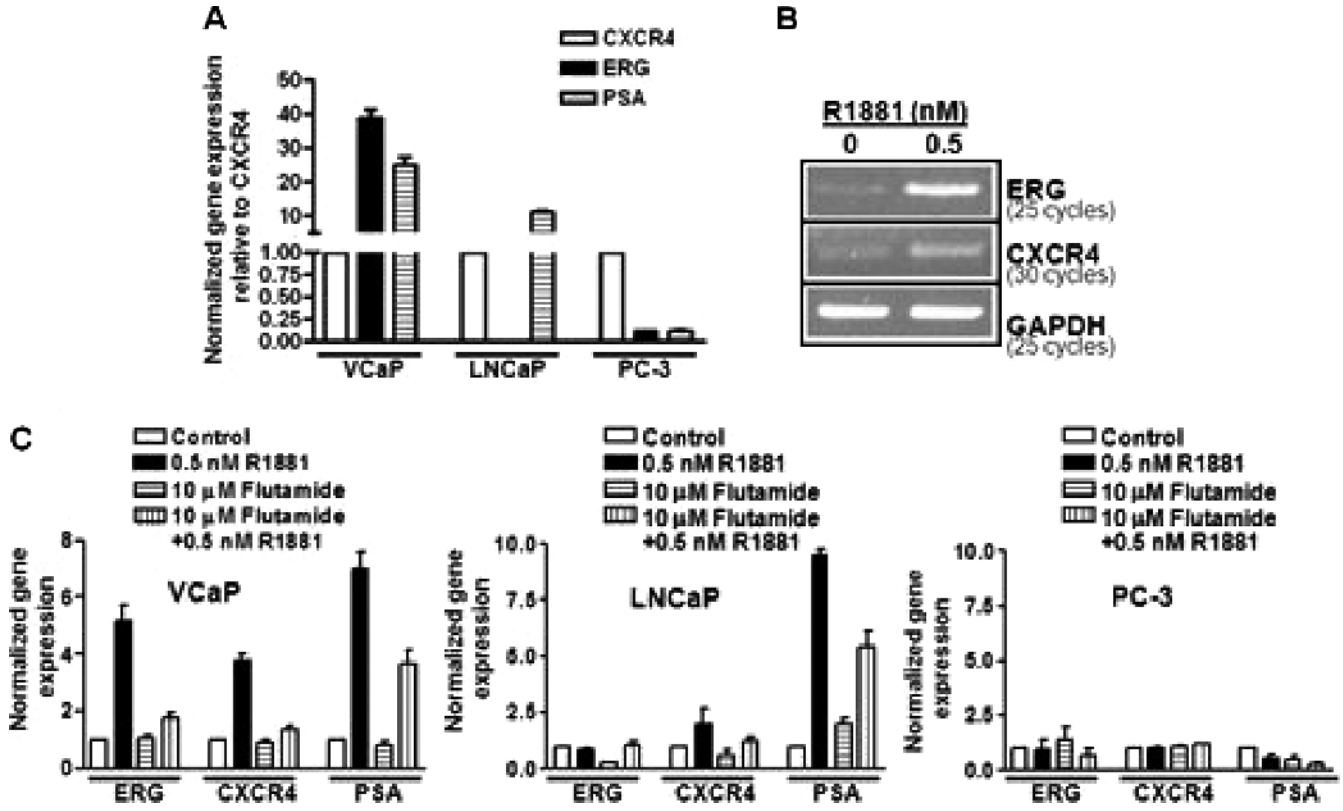

Figure 2. The synthetic androgen, R1881, induces ERG and CXCR4 expression in PC cells. (A) Relative gene expressions of *ERG*, *CXCR4*, and *PSA* are shown in PC-3, LNCaP, and VCaP cells. (B) R1881- and vehicle-treated VCaP cells were analyzed for *ERG*, *CXCR4*, and *GAPDH* gene expression. The PCR-amplified gene products were analyzed on ethidium bromide agarose gel. (C) PC-3, LNCaP, and VCaP cells treated with vehicle, R1881, flutamide, and a combination of both reagents were analyzed for *ERG*, *CXCR4*, *PSA*, and *GAPDH* gene expressions.

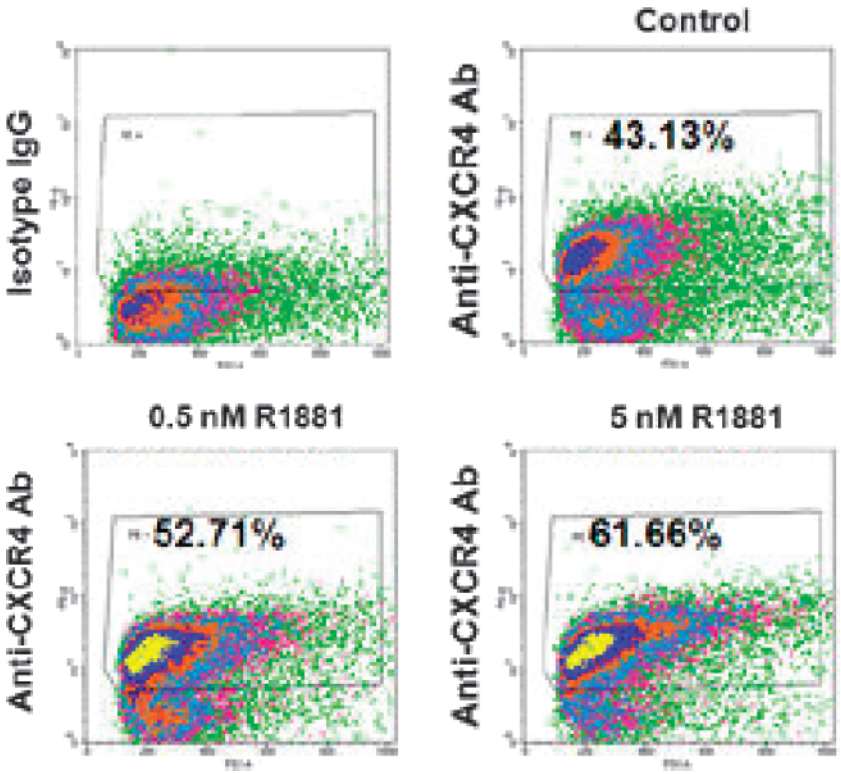

Figure 3. *CXCR4* is an androgen-responsive gene in VCaP cells. VCaP cells were treated with different concentrations of R1881, and cell surface expression of *CXCR4* was determined by FACS analysis.

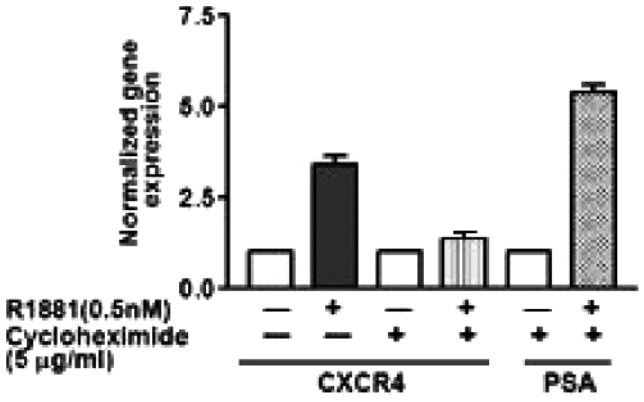

Figure 4. Cycloheximide abrogates R1881 induction of *CXCR4* gene expression. VCaP cells were treated with vehicle, R1881 (0.5 nM), cycloheximide (5 μg/ml), and a combination of cycloheximide and R1881. In the combination experiment, cycloheximide was initially treated with cells, and 1 hour later, R1881 was added. *CXCR4* and *PSA* gene expressions were determined by quantitative PCR. Fold differences in the gene expression were determined after normalization with *GAPDH* expression.

ERG-Mediated CXCR4 Expression Regulates PC Cell Chemoinvasion

We have previously shown that bone tissue associated CXCL12 is active in CXCR4-dependent PC cell chemoinvasion through the expression of matrix metallopeptidase-9 [17]. To assess the functional significance of ERG-mediated CXCR4 expression in VCaP cells, we performed *in vitro* chemoinvasion assays (Figure 6*A*). CXCL12 induced chemoinvasion of VCaP cells, which suggests that the CXCR4 expressed in these cells was active in chemoinvasion toward the CXCL12 gradient. Treatment of VCaP cells with R1881 also induced chemoinvasion compared with that in vehicle-treated cells. Interestingly, simultaneous exposure to both agents additively enhanced chemoinvasion of VCaP cells, suggesting that androgen-induced CXCR4 is active in the chemoinvasion of VCaP cells toward a CXCL12 gradient. To determine whether R1881-induced CXCR4 enhances VCaP cell chemoinvasion, we treated VCaP cells with the CXCR4 antagonist AMD3100. AMD3100 downregulated CXCL12/CXCR4–mediated VCaP cell chemoinvasion similar to the levels of R881 treatment (Figure 6*B*). Together, these data suggest that the androgen activation of TMPRSS2-ERG translocations contributes to PC cell chemoinvasion through CXCR4 expression and activation.

Discussion

Herein, we demonstrate that androgens induce CXCR4 gene expression in TMPRSS2-ERG–positive VCaP cells. To our knowledge, this is the first report identifying the *CXCR4* gene as a target for TMPRSS2-ERG activation in PC cells. In this study, we show that androgen-responsive VCaP cell lines coexpress higher levels of CXCR4 and ERG compared with androgen-unresponsive PC-3 cells. ERG protein expression is absent in PC-3 cells, whereas it is expressed in two forms by VCaP cells (Figure 1*B*) as was previously shown by Tomlins et al. [1]. The two ERG species expressed in VCaP cells are most likely due to the alternative splicing of the fusion transcript. There is significant heterogeneity in the expression of fusion transcripts in tumor cells with TMPRSS2-ERG

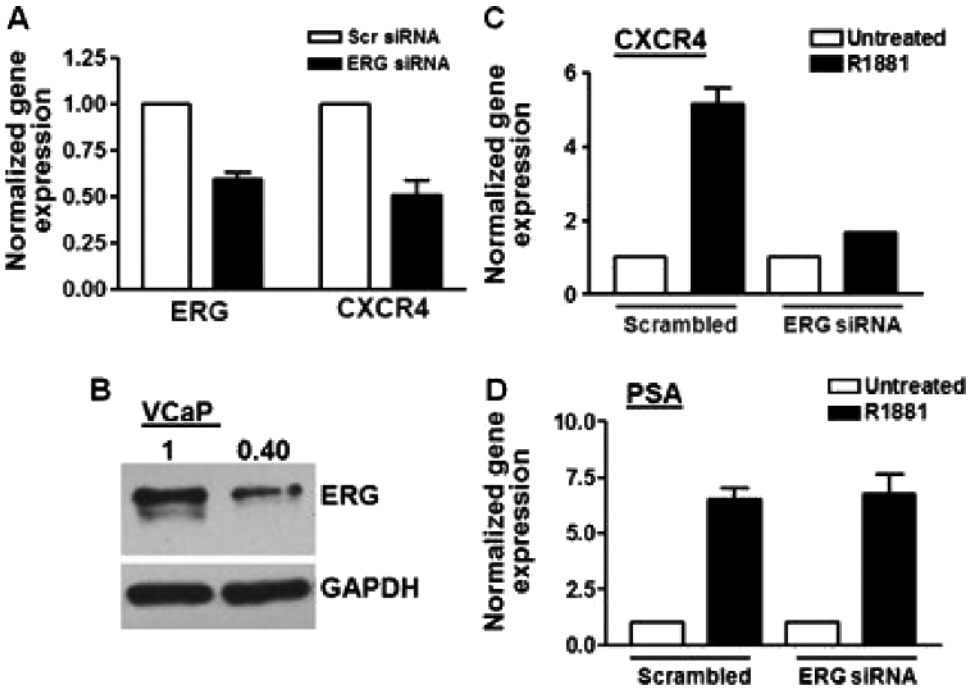

Figure 5. ERG factor mediates *CXCR4* expression in VCaP cells. (A) *ERG*, *CXCR4*, and *GAPDH* gene expressions were determined in scrambled (Scr) and ERG siRNA-transfected VCaP cells, and *ERG* and *CXCR4* gene expressions shown after normalization for *GAPDH*. (B) Scrambled and ERG siRNA-transfected VCaP cell lysates were immunoblotted with anti-ERG, anti-CXCR4 and anti-GAPDH antibodies. (C) Scr and ERG siRNA-transfected VCaP cells were treated with vehicle and R1881. Quantitative PCR analysis of *CXCR4* and *GAPDH* was performed. (D) *PSA* gene expression was analyzed in scrambled and ERG siRNA-transfected VCaP cells.

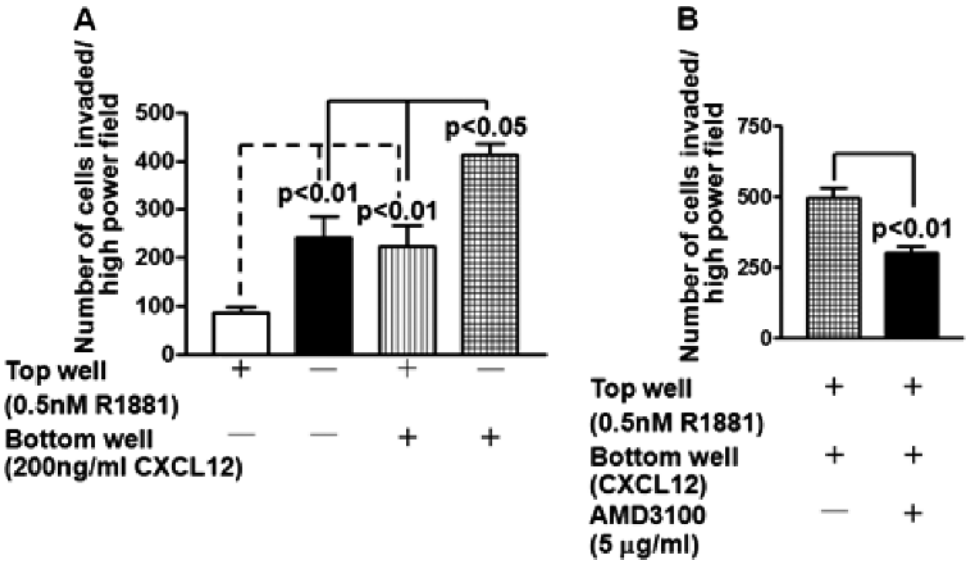

Figure 6. R1881 induced CXCR4 active in the chemoinvasion of VCaP cells: (A) VCaP cells were serum-starved, and chemoinvasion was performed using Matrigel-coated filters. CXCL12 was included in the bottom chamber as a chemoattractant. The cells were treated either with vehicle or with R1881 at 0.5 nM. (B) R1881-treated VCaP cells were further exposed to the *CXCR4* antagonist AMD3100, and chemoinvasion was performed in the presence of CXCL12.

alterations [1,7,27,28], and the translation of these transcripts could give rise to several ERG species. For example, these ERG forms can lack 39 amino acids at the N-terminus [1], fusion with the first five amino acids of TMPRSS2 protein and lack the N-terminus of ERG [7], have an insertion of 24 amino acids in the central domain of ERG [29], or have a deletion of the C-terminus Ets binding domain [27]. A recent study by King et al. [13] has shown that fast migrating ERG species in the doublet has been the translation product from the first AUG codon in the fourth exon. This translation product lacks 39 N-terminal amino acids. Overexpression studies in cell culture and animal models with several of these ERG forms, with the exception of the C-terminus Ets domain deletion, demonstrate that they play a key role in PC cell proliferation [29], invasion [9,10], and progression [12,13]. Overall, the data strongly indicate that activation and alterations of TMPRSS2-ERG contribute to the lethal characteristics of PC development in patients.

Previous studies show that similar TMPRSS2-ERG deletions are present in both primary tumor cells and disseminated metastatic cells to several secondary sites [30], which suggest that downstream target genes of TMPRSS2-ERG fusions facilitate the tumor cell invasion and dissemination process. Recent studies suggest that the chemokine receptor CXCR4 in tumor cells and its ligand CXCL12 expressed in secondary metastatic sites play a key role in the metastasis of primary tumor cells [16–18,25]. Our data support the notion that TMPRSS2-ERG activation in PC cells regulates CXCR4 expression and subsequent metastasis to secondary sites.

Our study shows that the synthetic androgen upregulates the ERG expression in fusion-positive VCaP cells, which is in line with findings previously reported by Tomlins et al. [1]. Interestingly, we found that CXCR4 is regulated in parallel with ERG in a panel of PC cells. In LNCaP cells, the synthetic androgen induced a very modest degree of *CXCR4* gene expression in (Figure 2*C*). Because LNCaP cells have very low levels of ERG in the absence of TMPRSS2-ERG translocations, this regulation could be mediated indirectly by additional AR-dependent processes. Alternatively, other Ets factors could contribute to CXCR4 expression in these cells. In support of the potential regulation by other Ets factors, ETV1 has been shown to be expressed in LNCaP cells [1] and could mediate CXCR4 expression through Ets binding sites in the CXCR4 promoter. Studies are in progress to identify the specific ERG and Ets binding sites in the CXCR4 promoter. The moderate levels of CXCR4 expression induced by R1881, coupled with the presence of ETV1 in these cells, support the notion that ERG and ETV1 translocations could be mutually exclusive in prostate tumor samples and could mediate prometastatic *CXCR4* gene expression, as well as the subsequent invasion and metastasis of tumor cells. In VCaP cells, androgen-induced CXCR4 expression is mediated by the overexpression of ERG rather than by the general growth effects of androgens because we did not observe changes in the CXCR4 expression in VCaP cells in the presence of serum (data not shown).

CXCR4 has been shown to be regulated at the transcriptional level by the growth factor through hypoxic [31] and nuclear factor κB transcription factor activities [32]. In contrast with those models, our data with cycloheximide (Figure 3) suggest that androgen-mediated protein synthesis is required for CXCR4 expression in PC cells. Furthermore, such a requirement is only present in PC cells exhibiting the TMPRSS2-ERG translocations. Our analysis (data not shown) suggests that CXCR4 promoter does not contain consensus AR binding sites [33], and thus, this regulation is most likely to be mediated indirectly. Conversely, Akashi et al. [34] have shown that overexpression of AR in DU145 cells down-regulated CXCR4 expression, although it is not clear whether the overexpressed AR is active in these cells. Although the lack of an AR binding site in the CXCR4 promoter region suggests that such down-regulation could be indirectly mediated by AR activation, which would be independent of ERG function in these cells, overexpression of ERG in TMPRSS2-ERG fusion–positive cells could override these inhibitory effects on CXCR4 expression.

In agreement with our conclusions, Carver et al. [12] recently reported, while this article was in preparation, that ERG-transfected PC-3 cells have higher functional CXCR4 expression. Our data also demonstrate that *CXCR4* is a target gene for the ERG transcription factor, and our results with the synthetic androgen regulation of CXCR4 (Figure 2) further

suggest that CXCR4 is a physiological target of androgens in prostate tumor cells and that this process could facilitate the pathological progression of tumor cell metastasis through the CXCL12/CXCR4 axis. Carver et al. reported that ERG binds to Ets binding sites in the −2683 to −2531 promoter of CXCR4, whereas the data from chromatin immunoprecipitation analysis in this study identified ERG binding sites in the CXCR4 promoter between the transcription start site and the −513 of the CXCR4 promoter. We identified eight potential ERG binding sites in the 1-kb CXCR4 promoter, and three of these putative sites were present in the transcription start site to the −513 of the CXCR4 promoter. Maroni et al. [35] reported that Ets1 factor binds to −397 to −412 and −478 to −481 sites in the CXCR4 promoter, suggesting that Erg could also bind to these sequences. Because ERG is under androgen control in TMPRSS2-ERG–positive cells, it is highly likely that ERG could be the relevant factor interacting with the CXCR4 promoter in PC cells. The sequences between −513 and −996 have four potential ERG binding sites, but our attempts to design primers to amplify this region have been unsuccessful so far because of the high percentage of GC content at this region. Studies are in progress to determine the relative contribution of these putative ERG binding sites in the regulation of the CXCR4 promoter.

ERG knock down by siRNA has been shown to decrease invasive and proliferative functions in VCaP cells. Our previous data demonstrated that the CXCL12/CXCR4 axis promotes PC cell invasion through activation of signaling pathways leading to protease expression [17]. CXCR4 expression also has been shown to contribute to the growth of tumor cells in bone metastatic sites [18]. Our present data demonstrate that ERG knockdown attenuates androgen-dependent CXCR4 expression without significantly changing *PSA* expression. These results suggest that the TMPRSS2-ERG fusion facilitates tumor cell invasion and metastasis through the regulation of CXCR4 expression and function in PC cells. To test this concept, our data with an *in vitro* invasion assay (Figure 6) demonstrate that R1881 alone can induce VCaP cell invasion. This supports previously published reports that R1881-induced ERG expression contributes to *in vitro* invasion of VCaP cells and is mediated by the expression of proteases [9,10]. Interestingly, the R1881-treated cells invaded more efficiently in the presence of CXCL12. CXCR4 inhibition suppressed the CXCL12 effect, suggesting that androgen-induced CXCR4 expression is functional in VCaP cells and contributes to PC cell invasion. These data are in line with previous reports, demonstrating the role of ERG in CXCR4 function in PC cells [12].

In summary, we show that TMPRSS2-ERG activation in fusion-positive cancer cells induces the expression of the prometastatic gene *CXCR4*, which is functionally active in the chemoinvasion process. Targeting *CXCR4*, a relevant target for androgen activation of TMPRSS2-ERG, could be an advantageous strategy for lethal phenotypes associated with these chromosomal translocations in PC patients.

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Table W1. ETS/ERG Binding Sites in CXCR4 Promoter.

Nucleotide Position Relative to Transcription Start Site in CXCR4 Promoter	Nucleotide Sequence
–119 to –126	GA**GGAA**GC
–234 to –241	TA**GGAA**AT
–420 to –417	GC**GGA**TGT
–513 to –520	AA**GGAA**GT
–700 to –707	TA**GGAT**AA
–850 to –857	CA**GGAA**GT
–889 to –896	GC**GGA**TCT
–919 to –926	CC**GGAA**GA
–2517 to –2525	CT**GGAA**TT
–2664 to –2656	GG**GGAA**TG

ETS core sequence: **GGA(A/T)**.
ERG consensus sequence: (C/A)**GGAA**(G/A)T.